L Number	Hits	Search Text	DB	Time stamp
1	36028	eluent	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:23
2	7489	immobiliz$ adj antibod$3	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:24
3	73095	mass adj spectr$	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:24
4	205	eluent and (immobiliz$ adj antibod$3)	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:24
6	19	((mass adj spectr$) and (eluent and (immobiliz$ adj antibod$3))) and maldi	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:29
7	4936	elut$ and (immobiliz$ adj antibod$3)	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:30
8	868	(mass adj spectr$) and (elut$ and (immobiliz$ adj antibod$3))	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:30
9	143	((mass adj spectr$) and (elut$ and (immobiliz$ adj antibod$3))) and maldi	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:30
5	53	(mass adj spectr$) and (eluent and (immobiliz$ adj antibod$3))	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 15:30

L Number	Hits	Search Text	DB	Time stamp
1	34107	affinity adj chromatography	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 09:51
2	56562	mass adj spectro$	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 09:51
3	490	(affinity adj chromatography) same (mass adj spectro$)	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 10:00
4	7195	2.ti.	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 10:00
5	145	2.ti. and antibod$3	USPAT; US-PGPUB; EPO; DERWENT	2004/05/27 10:25
6	1	("4527059").PN.	USPAT; US-PGPUB	2004/05/27 10:25
7	1	(("4527059").PN.) and (molecular adj weight)	USPAT; US-PGPUB	2004/05/27 10:28
8	1	("5643800").PN.	USPAT; US-PGPUB	2004/05/27 10:29
9	0	(("5643800").PN.) and (molecular adj weight)	USPAT; US-PGPUB	2004/05/27 10:29
10	0	(("5643800").PN.) and mw	USPAT; US-PGPUB	2004/05/27 10:32
11	1	(("5643800").PN.) and antibod$3	USPAT; US-PGPUB	2004/05/27 10:44
12	1	("5891742").PN.	USPAT; US-PGPUB	2004/05/27 10:44
13	1	(("5891742").PN.) and (molecular adj weight)	USPAT; US-PGPUB	2004/05/27 10:44

L18 ANSWER 94 OF 100 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 49

TI Matrix-assisted laser desorption ionization for rapid determination of the sequences of biologically active peptides isolated from support-bound combinatorial peptide libraries

AB A termination synthesis approach has been developed to encode each resin **bead** in support-bound combinatorial peptide libraries with the information needed to establish the sequence of the full-length products also contained on the beads. Matrix-assisted laser desorption ionization **mass spectrometry** was then used to rapidly read the appropriate sequences. In addn. to rapid peptide sequencing, the technique allows direct assessment of the quality of the synthetic library, since deletion peptides, side-reaction products and incomplete-deprotection products are readily obsd. An anti-gp120 monoclonal **antibody** was screened against a hexapeptide library, and eight active peptides are isolated. Six of the eight peptides were shown to possess the exact recognition sequence for the **antibody** .

SO Rapid Communications in Mass Spectrometry (1994), 8(1), 77-81
CODEN: RCMSEF; ISSN: 0951-4198

AU Youngquist, R. Scott; Fuentes, Gary R.; Lacey, Martin P.; Keough, Thomas

L7 ANSWER 55 OF 58 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN

TI LASER-DESORPTION TIME-OF-FLIGHT MASS-SPECTROMETRIC ANALYSIS OF TRANSFERRIN PRECIPITATED WITH ANTISERUM - A UNIQUE SIMPLE METHOD TO IDENTIFY MOLECULAR-WEIGHT VARIANTS

AB Serum transferrin precipitated with anti-transferrin serum was analysed by matrix-assisted laser desorption ionization time-of-flight mass spectrometry (**MALDI**-TOFMS). The transferrin-**antibody** complex in the immuno-precipitates was separated into transferrin and IgG in an acidic pH, which is the usual condition of loading on **MALDI** -TOFMS. Ions of IgG and other minor components were not superimposed on the transferrin ions. Transferrin isoforms with different carbohydrate contents could be identified by this simple method easier than by **affinity** chromatography requiring the time-consuming preparation of an insolubilized specific **antibody**. The transferrin isoform with a molecular weight of similar to 2.2 kDa smaller than normal transferrin, which is contained in the serum from patients with carbohydrate-deficient glycoprotein (CDG) syndrome, was identified by this method In addition to the M(1+) ion detected using sinapinic acid as a matrix, the M(2+) and M(3+) ions of transferrin were clearly detected using alpha-cyano-4-hydroxycinnamic acid as matrix and the molecular weight heterogeneity was identified more clearly in multivalent ions than that in the M(1+) ion. The **MALDI**-TOF analysis of immuno-precipitates may serve as a simple and sensitive method to identify the molecular weight heterogeneity of various biological materials.

SO BIOLOGICAL MASS SPECTROMETRY, (APR 1994) Vol. 23, No. 4, pp. 230-233. ISSN: 1052-9306.

AU NAKANISHI T; OKAMOTO N; TANAKA K; SHIMIZU A (Reprint)